

Serial No. 09/311,689  
Group Art Unit: 1652

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-8. (Cancelled)

9. (Currently Amended) [A] An isolated polypeptide with at least 30% sequence identity to the polypeptide of Seq. ID No. 2 and comprising greater than fifty amino acids in length and modified in order to have a composition selected from ~~one of the~~ following: at least 5-15 mole % methionine, at least 6-25 mole % threonine, and at least 4-9 mole % tryptophan, or a combination thereof; wherein the % sequence identity is based on the entire sequence and is determined by BLAST 2.0 using default parameters.

10. (Currently Amended) [A] An isolated polypeptide comprising Seq. ID No. 2 or 4 that has been modified to substitute ~~contain seven or more~~ non-native essential amino acid residues at seven or more positions corresponding to the positions in Seq. ID No. 2 selected from 1, 8, 11, 17, 18, 19, 20, 22, 23, 31, 34, 38, 40, 41, 47, 49, 56, 58, 59, 60, 61, 62, 63, 65, 67, 69, 73, 75, 76, 78, 79, 81, or 82 ~~or combinations thereof~~, and further provided that the polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 2 or 4, wherein the percent identity is determined by Blast 2.0 using default parameters wherein native residues are those in the unsubstituted sequence.

11-18. (Cancelled)

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19. (Currently Amended) [A] An isolated polypeptide comprising Seq. ID No. 2 that has been modified to contain two or more substitutions ~~modifications, said two or more modifications corresponding to positions in Seq. ID No. 2~~ selected from the group consisting of:

H18A, H18I, H18L, H18V, H18M, N19K, N19T, L20M, L20I, L20V, E23T, E23K, S31T, S32K, E34K, E34T, V38M, V38I, V38L, L40M, L40I, L40V, Q41K, Q41T, Q47K, Q47T, I49M, I49I, I49L, I49V, I56K, I56T, M59G, R62K, R62T, I63M, I63L, I63V, R65K, R65T, R67K, R67T, F69W, L73K, L73T, N75K, N75T, Q78K, Q78T, V79T, V79K, R81K, and R81T; and

further provided that the polypeptide is a nutritional supplement ~~and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.~~

20. (Cancelled)

21. (Currently Amended) [A] An isolated polypeptide comprising Seq. ID No. 2 that has been modified to contain two or more substitutions ~~modifications, said two or more modifications corresponding to positions in Seq. ID No. 2~~ selected from the group consisting of:

H18A, H18M, N19K, L20M, T22C, E23T, E23C, S31T, E34K, V38M, L40M, Q41K, Q47K, I49M, I56K, M59G, R62K, I63M, R65K, R67K, F69W, L73K, N75K, Q78K, V79T, R81K, R81C, and V82C; and

further provided that the polypeptide is a nutritional supplement ~~and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.~~

22-27. (Cancelled)

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28. (Currently Amended) [A] An isolated polypeptide comprising Seq. ID No. 2 modified to contain three or more substitutions ~~modifications~~, said three or more substitutions ~~modifications~~ comprising non-native essential amino acids replacing native amino acids at positions ~~corresponding to Seq. ID No. 2 and~~ selected from the group consisting of positions

1, 8, 11, 17, 18, 19, 20, 22, 23, 31, 32, 34, 38, 40, 41, 45, 47, 49, 56, 58, 59, 60, 61, 62, 63, 64, 65, 67, 69, 73, 74, 75, 76, 77, 78, 79, 81 and 82; and excluding V and W at position 56; K, V and W at position 58; W, V and K at position 59; T, I and K at position 60; V and W at position 61 and V and F at position 62; and

further provided that the polypeptide is a nutritional supplement ~~and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.~~

29. (Currently Amended) An isolated polypeptide comprising Seq. ID No. 6, 8, 10, 12, 14, 16, 18, 20 or conservative substitutions ~~a conservatively substituted polypeptide thereof, wherein said isolated polypeptide or conservative substitutions conservatively substituted polypeptide thereof have~~ has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

30. (Cancelled)

31. (Currently Amended) An isolated polypeptide providing an increased level of essential amino acids with respect to SEQ ID NO:2, with more than 79% sequence identity to the polypeptide of Seq. ID No. 20, and comprising greater than fifty amino acids in length and modified in order to have a composition selected from the following: at least 5-15 mole % methionine, at least 6-25 mole % threonine, and at least 4-9 mole % tryptophan, or a combination thereof; wherein the percent

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sequence identity is determined by GAP analysis using Gap Weight of 12 and Length Weight of 4.

32-53. (Cancelled)

54. (Previously Presented) The polypeptide of claim 9, wherein the polypeptide is modified in order to have a composition of at least 5-15 mole % methionine.

55. (Previously Presented) The polypeptide of claim 9, wherein the polypeptide is modified in order to have a composition of at least 6-25 mole % threonine.

56. (Currently Amended) The polypeptide of claim 10 wherein the non-native essential amino acid residues comprise lysine and the positions correspond to the positions in Seq. ID No. 2 selected from 1, 8, 11, 17, 19, 34, 41, 56, 59, 62, 65, 67, or 73 or combinations thereof.

57. (Currently Amended) Food or feed comprising the polypeptide of claim ~~30~~ 9.

58. (Original) Food or feed comprising the polypeptide of claim 31.

59-60. (Cancelled)

61. (Previously Presented) An isolated polypeptide comprising Seq. ID Nos. 6, 8, 10, 12, 14, 16, 18 or 20.

62-75 (Cancelled)

76. (Previously Presented) [A] An isolated polypeptide comprising Seq. ID No. 4, ~~that wherein said polypeptide~~ has been modified to contain at least eleven non-

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native essential amino acids, and modified in order to have a composition selected from the following: at least 5-15 mole % methionine, at least 6-25 mole % threonine, and at least 4-9 mole % tryptophan, or a combination thereof; and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 4, the percent sequence identity determined by Blast 2.0 using default parameters.

77-99. (Cancelled)